

Does Not Comply
Corrected Diskette Needed

1646

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 07/17/2000

PATENT APPLICATION: US/09/170,980A

TIME: 16:31:35

Input Set : A:\PF01951DIVSEQLST.txt

Output Set: N:\CRF3\07172000\I170980A.raw

3 <110> APPLICANT: Hillman, Jennifer L.
4 Goli, Surya K.
6 <120> TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED KALLIKREIN
8 <130> FILE REFERENCE: PF-0195-1 DIV
10 <140> CURRENT APPLICATION NUMBER: 09/170,980A
11 <141> CURRENT FILING DATE: 1998-10-13
13 <150> PRIOR APPLICATION NUMBER: 08/790,137
14 <151> PRIOR FILING DATE: 1997-01-29
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PERL Program
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 253
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: unsure
27 <222> LOCATION: 54, 55
28 <223> OTHER INFORMATION: unknown, or other
W--> 30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <223> OTHER INFORMATION: SEQ ID NO:1
34 <400> SEQUENCE: 1
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36 1 5 10 15
37 Gly Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu
38 20 25 30
39 Cys Glu Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr Gln Lys
40 35 40 45
41 Thr Arg Leu Leu Cys Gly Ala Thr ~~Xaa~~ Xaa Ala Pro Arg Trp Phe
42 50 55 60
43 Leu Thr Ala Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu
44 65 70 75
45 Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg
46 80 85 90
47 Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu
48 95 100 105
49 Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala
50 110 115 120
51 Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser
52 125 130 135
53 Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp
54 140 145 150
55 Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg
56 155 160 165
57 Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
58 170 175 180
59 Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln

← L2207 Feature: must be
left blank, with no
extraneous markers.

See p. 2

RAW SEQUENCE LISTING

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Input Set : A:\PF01951DIVSEQLST.txt

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60          185          190          195
61 Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
62          200          205          210
63 Val Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp
64          215          220          225
65 Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys
66          230          235          240
67 Lys Tyr Val Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
68          245          250
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 833
73 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapiens
W--> 76 <220> FEATURE: - Same as p.1
77 <221> NAME/KEY: misc_feature
78 <223> OTHER INFORMATION: SEQ ID NO: 2
80 <400> SEQUENCE: 2
81 gctggccctt ggacacctet gtcaccatgt ggttctctgt tctgtgcctc gccctgtccc 60
82 tggggggggac tgggtctgctg ccccccattc agtcccggat tgtggggaggc tgggagtgtg 120
83 agcagcattc ccagccctgg caggcggtc tgtaccagaa gacgcggcta ctctgtgggg 180
W--> 84 cgacgctcat cccccccaga tgggttctga cagcagccca ctgcttgaag ccccgctaca 240
85 tagttcacct ggggcagcac aacctccaga aggaggagg ctgtgagcag acccggtacag 300
86 ccaactgagtc cttccccac cccggcttca acaacagcct ccccaacaaa gaccaccgca 360
87 atgacatcat gctggtgaag atggcatcgc cagtctccat cacttgggtc gtgcgacccc 420
88 tcaccctctc ctcacgctgt gtcactgtg gcaccagctg cctcatttcc ggcctggggca 480
89 gcacgtccag cccccagtta cgctgtcctc acaccttgcg atgcgccaac atcaccatca 540
90 ttgagcacca gaagtgtgag aacgcctacc ccggcaacat cacagacacc atggtgtgtg 600
91 ccagcgtgca ggaagggggc aaggactcct gccagggtga ctccgggggc cctctggtct 660
92 gtaaccagtc tcttcaaggc attatctcct ggggccagga tccgtgtgct atcacccgaa 720
93 agcctggtgt ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 780
W--> 94 acaattagac tggacgtcac ctccgaatcc cccacagccc atcacctctc att 833
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 262
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
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102 <222> LOCATION: GenBank
103 <223> OTHER INFORMATION: g186653
105 <400> SEQUENCE: 3
106 Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr
107 1 5 10 15
108 Gly Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu
109 20 25 30
110 Cys Glu Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe
111 35 40 45
112 Ser Thr Phe Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val
113 50 55 60
114 Leu Thr Ala Ala His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu
115 65 70 75

```

→ Missing mandatory <222>
Location feature. Locations
of n's in sequence
must be specified.
See #10 on
Error Summary Sheet

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/170,980A

DATE: 07/17/2000
 TIME: 16:31:35

Input Set : A:\PF01951DIVSEQLIST.txt
 Output Set: N:\CRF3\07172000\I170980A.raw

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116 Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr Ala Gln Phe Val
117                               80                85                90
118 His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn Met Ser Leu
119                               95                100               105
120 Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser His Asp
121                               110               115                120
122 Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr Asp
123                               125                130                135
124 Ala Val Lys Val Val Glu Leu Pro Thr Gln Glu Pro Glu Val Gly
125                               140                145                150
126 Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn
127                               155                160                165
128 Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu
129                               170                175                180
130 Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys Val Thr Asp
131                               185                190                195
132 Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys
133                               200                205                210
134 Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln
135                               215                220                225
136 Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
137                               230                235                240
138 Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu
139                               245                250                255
140 Asp Thr Ile Ala Glu Asn Ser
141                               260
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 263
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <220> FEATURE:
150 <222> LOCATION: GenBank
151 <223> OTHER INFORMATION: g55527
153 <400> SEQUENCE: 4
154 Met Trp Phe Leu Ile Leu Phe Leu Ala Leu Phe Leu Gly Gly Ile
155 1 5 10 15
156 Asp Ala Ala Pro Pro Val Gln Ser Arg Ile Ile Gly Gly Phe Asn
157 20 25 30
158 Cys Glu Lys Asn Ser Gln Pro Trp His Val Ala Val Tyr Arg Phe
159 35 40 45
160 Ala Arg Tyr Gln Cys Gly Gly Val Leu Leu Asp Ala Asn Trp Val
161 50 55 60
162 Leu Thr Ala Ala His Cys Tyr Asn Asp Lys Tyr Gln Val Trp Leu
163 65 70 75
164 Gly Lys Asn Asn Arg Phe Glu Asp Glu Pro Ser Ala Gln His Gln
165 80 85 90
166 Leu Ile Ser Lys Ala Ile Pro His Pro Gly Phe Asn Met Ser Leu
167 95 100 105
168 Leu Asn Lys Asp His Thr Pro His Pro Glu Asp Asp Tyr Ser Asn

```

w-->

Same as p.1

RAW SEQUENCE LISTING DATE: 07/17/2000
 PATENT APPLICATION: US/09/170,980A TIME: 16:31:35

Input Set : A:\PF01951DIVSEQLST.txt
 Output Set: N:\CRF3\07172000\I170980A.raw

169		110		115		120
170	Asp Leu Met Leu Val Arg Leu Lys Lys	Pro Ala Glu Ile Thr Asp				
171		125		130		135
172	Val Val Lys Pro Ile Asp Leu Pro Thr	Glu Glu Pro Thr Val Gly				
173		140		145		150
174	Ser Arg Cys Leu Ala Ser Gly Trp Gly	Ser Thr Thr Pro Thr Glu				
175		155		160		165
176	Glu Phe Glu Tyr Ser His Asp Leu Gln Cys	Val Tyr Leu Glu Leu				
177		170		175		180
178	Leu Ser Asn Glu Val Cys Ala Lys Ala His	Thr Glu Lys Val Thr				
179		185		190		195
180	Asp Thr Met Leu Cys Ala Gly Glu Met Asp	Gly Gly Lys Asp Thr				
181		200		205		210
182	Cys Val Gly Asp Ser Gly Gly Pro Leu Ile	Cys Asp Gly Val Leu				
183		215		220		225
184	Gln Gly Ile Thr Ser Trp Gly Pro Thr Pro	Cys Ala Leu Pro Asn				
185		230		235		240
186	Val Pro Gly Ile Tyr Thr Lys Leu Ile Glu	Tyr Arg Ser Trp Ile				
187		245		250		255
188	Lys Asp Val Met Ala Asn Asn Pro					
189		260				

VERIFICATION SUMMARY DATE: 07/17/2000
PATENT APPLICATION: US/09/170,980A TIME: 16:31:36

Input Set : A:\PF01951DIVSEQLIST.txt
Output Set: N:\CRF3\07172000\I170980A.raw

L:25 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:84 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:84 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:94 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:101 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:149 M:256 W: Invalid Numeric Header Field, <220> has non-blank data

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7.

Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/170,980 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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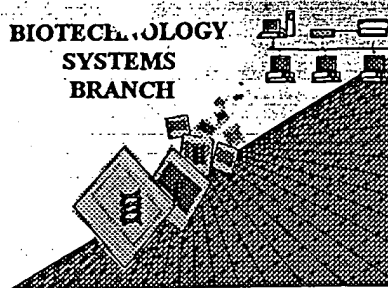
AUG 08 2000

TECH CENTER 1600/2900

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1646

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



#9
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AUG 08 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/170,980 A

Source: 1646

Date Processed by STIC: 7-17-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>